(i) Printed Pages : 3 Roll No. .....

(ii) Questions : 9 Sub. Code : 1 7 9 8 3

Exam. Code : 0 0 3 7

B.Sc. (Hons.) Biotechnology 5th Semester

(2124)

BIOINFORMATICS (Common with Tools in Bioinformatic)

Paper : BIOT-503-T

Time Allowed : Three Hours] **[Maximum Marks : 67**

Note :— Attempt **five** questions in all. Q. No. **1** is compulsory. Select **one** question each from Unit-I to Unit-IV.

1. Answer the following :

   (a) Define INSDC.

   (b) What is BLASTx ?

   (c) What are substitution matrices ?

   (d) What does 45 signify in BLOSUM45 ?

   (e) Explain Affine Gap Penalty.

   (f) Define Log Odd Ratio.

   (g) Differentiate between rooted and unrooted trees.

   (h) Define Polytomy trees.

   (i) Define Genome annotation.

   (j) What are Rotamers ? Give example of a Rotamer library.

10×1½

UNIT—I

2. (a) Explain the need of Bioinformatics technology in Biological Sciences.

   (b) What are Primary Sequence Databases ? Explain briefly GenBank. 6+7

3. (a) Differentiate between SCOP and CATH. 3

   (b) Write short notes on the following :

   (i) PDB (ii) pfam 10

UNIT—II

4. (a) Explain DOTPLOT method of sequence alignment.

   (b) Write in detail about algorithm of BLAST sequence alignment tool. 6+7

5. (a) Explain the Smith Waterman pair wise sequence alignment method with suitable example.

   (b) Explain Hierarchical method of multiple sequence alignment. 6+7

UNIT—III

6. (a) Give different tree topologies and terminologies used in molecular phylogeny.

   (b) Explain with example the UPGMA method of phylogenetic tree construction. 6+7

7. (a) Explain maximum Parsimony method of phylogenetic tree construction.

   (b) Give applications of Phylogenetic Analysis.

   (c) Write a note on Phylip. 7+3+3

UNIT—IV

8. (a) Write note on methods of gene prediction in prokaryotes.

   (b) Write note on protein 2° structure prediction methods.

6+7

9. (a) Give features and applications of Rasmol.

   (b) Explain the concept of Homology Modeling to predict the protein 3° structures.

6+7